IN THE UNITED STATES PATENT & TRADEMARK OFFICE

In re Application	:	Mats Hellström et al.
Serial No.	:	10/581,761
Filed	:	June 5, 2006
For	:	ANGIOGENESIS AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF
Examiner	:	
Attorney Docket	:	102959-202
Group Art Unit	:	1653
Confirmation No.	:	6588
Customer No.	:	27267

* *

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: Mail Stop PCT, Commissioner for Patents, P. O. Box 1450, Alexandria, Virginia 22313-1450 on 29 MAY 2008, 2008.

By Todd E. Garabedian

Todd E. Garabedian, Ph.D.
Registration No. 39,197
Attorney for Applicants

* *

Mail Stop PCT
Office of PCT Legal Administration
P.O. Box 1450
Alexandria, VA 22313-1450

RENEWED PETITION UNDER 37 CFR §1.137(b)

Dear Sir:

Applicants hereby respectfully request reconsideration of a decision to dismiss a Petition for revival of an unintentionally abandoned application under 37 CFR § 1.137(b).

A Dismissal of Petition to revive the PCT application PCT/SE2004/001814 was mailed May 6, 2008. Specifically, the Examiner notes that while applicants have submitted a properly executed declaration, the copy of the sequence listing in computer-readable form is flawed.

To address the errors noted by the Dismissal, Applicants submit herewith a substitute copy of the sequence listing in computer-readable form (CRF). A paper copy of the sequence listing is also enclosed. Applicants herein request the sequence listing be entered into the above-identified application.

Applicants state that with regard to the Sequence Listing, the information recorded in computer readable form is identical to the written sequence listing. Applicants submit no new matter is added herewith.

While Applicants believe no fee is currently due, Applicants authorize the Office to charge Deposit account 23-1665 for any fees due with respect to this renewed petition.

If the Examiner believes a telephone conference would aid in the continued prosecution of this application, the Examiner is

invited and encouraged to contact Applicants' representative at the telephone number listed below.

Respectfully submitted,

Mats Hellström, et al.

Date: 29 MAY 2008

By Todd E. Garabedian

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\18516\10\59303.1

SEQUENCE LISTING

<110> Hellstrom, Mats
Wallgard, Elisabeth
Kalen, Mattias

<120> ANGIOGENESIS AFFECTING POLYPEPTIDES,
PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF

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Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
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Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
65                  70                  75                  80
His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
                85                  90                  95
Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
            100                 105                 110
His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
        115                 120                 125
Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
    130                 135                 140
Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
145                 150                 155                 160
Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
                165                 170                 175
Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
            180                 185                 190
Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
        195                 200                 205
Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
    210                 215                 220
Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
225                 230                 235                 240
Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
                245                 250                 255
Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
            260                 265                 270
Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu
        275                 280                 285
Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp
    290                 295                 300
Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly
305                 310                 315                 320
Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe
                325                 330                 335
Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly
            340                 345                 350
Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln
        355                 360                 365
Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu
    370                 375                 380
Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys
385                 390                 395                 400
Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala
                405                 410                 415
Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu
            420                 425                 430
Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro
        435                 440                 445
Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr
    450                 455                 460
Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Gln Leu
```

```
465                 470                 475                 480
Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr
                485                 490                 495
Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg
            500                 505                 510
Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg
        515                 520                 525
Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
    530                 535                 540
Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met
545                 550                 555
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<210> 11
<211> 676
<212> DNA
<213> Murinae

<220>
<221> misc_feature
<222> 604
<223> n is a, c, g, or t

<400> 11
ggagctggtg ggccggagcg gcggcgccgc catgtccgac agcgagaagc tcaacctgga 60
ctccatcatc gggcgcctgc tggaagtgca gggctcacgg cctgggaaga acgtgcagct 120
gacagagaac gagatccgtg gtctgtgcct caaatcccgg gagattttcc tgagccagcc 180
cattcttctg gagcttgagg cgcccctcaa gatctgtggt gacatccatg gccagtacta 240
tgaccttcta cggctgtttg agtatggtgg cttccctcca gagagcaact acctcttctt 300
gggggattat gtagatcggg gcaagcagtc tttggagacc atctgcctgt tgctggccta 360
taagatcaga tacccggaga atttctttct acttcgtggg aaccatgagt gtgccagcat 420
caaccgcatt tatggcttct atgatgaatg caagagaaga tacaacatca aactgtggaa 480
gacgttcact gactgcttca actgcctgcc cattgcagcc attgtggatg agaagatctt 540
ctgctgccac gggggcctgt ctccagactt gcaatccatg gagcagatta ggcgtattat 600
gcgngccaca gacgtgcctg accagggcct actgtgtgat ctcctgtggt ctgaccctga 660
caagaaatag cctcca   676

<210> 12
<211> 1369
<212> DNA
<213> Murinae

<400> 12
ggaggcagga gagggcccgg agctggtggg ccggagcggc ggcgccgcca tgtccgacag 60
cgagaagctc aacctggact ccatcatcgg gcgcctgctg gaagtgcagg gctcacggcc 120
tgggaagaac gtgcagctga cagagaacga gatccgtggt ctgtgcctca aatcccggga 180
gattttcctg agccagccca ttcttctgga gcttgaggcg cccctcaaga tctgtggtga 240
catccatggc cagtactatg accttctacg gctgtttgag tatggtggct tccctccaga 300
gagcaactac ctcttcttgg gggattatgt agatcggggc aagcagtctt tggagaccat 360
ctgcctgttg ctggcctata agatcagata cccggagaat ttctttctac ttcgtgggaa 420
ccatgagtgt gccagcatca accgcattta tggcttctat gatgaatgca agagaagata 480
caacatcaaa ctgtggaaga cgttcactga ctgcttcaac tgcctgccca ttgcagccat 540
tgtggatgag aagatcttct gctgccacgg gggcctgtct ccagacttgc aatccatgga 600
gcagattagg cgtattatgc ggcccacaga cgtgcctgac cagggcctac tgtgtgatct 660
cctgtggtct gaccctgaca aggatgttca aggctggggc gagaatgacc gtggtgtctc 720

ctttaccttt ggggctgagg tggtagccaa gttcctgcac aagcatgatt tggacctcat 780
ctgcagagca catcaggttg tagaagatgg ctatgagttc tttgccaaga gacagttggt 840
gacactcttc tcagctccca actactgtgg agagtttgac aatgctggtg ccatgatgag 900
tgtggatgag accctcatgt gttccttcca gatcctcaag cccgctgata agaataaggg 960
caagtatggg cagttcagcg gcctgaaccc cggaggccgg cccatcactc caccccgcaa 1020
ttctgccaaa gccaagaaat agcctccatg tgctgccctt ctgccccaga tcgtttgtac 1080
agaaatcatg ctgccatggg tcacactggc ctctcaggcc cacccgtcac ggggaacaca 1140
cagcgttaag tgtctttcct ttatttttta aagaatcaat agcagcatct aatctcccag 1200
ggctccctcc caccagcacc tgtggtggct gcaagtggaa tcctggggcc aaggctgcag 1260
ctcagggcaa tggcagacca gattgtgggt ctccagcctt gcatggctgg cagccagatc 1320
ctggggcaac ccatctggtc tcttgaataa aggtcaaagc tggattctc 1369

<210> 13
<211> 330
<212> PRT
<213> Murinae

<400> 13
Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
 1   5   10   15
Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
            20   25   30
Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35   40   45
Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50   55   60
Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65   70   75   80
Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85   90   95
Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100   105   110
Arg Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115   120   125
Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130   135   140
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145   150   155   160
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165   170   175
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180   185   190
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195   200   205
Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210   215   220
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225   230   235   240
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245   250   255
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260   265   270
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275   280   285
Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly

```
    290                 295                 300
Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305                 310                 315                 320
Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
                325                 330
```

<210> 14
<211> 993
<212> DNA
<213> Homo sapiens

<400> 14
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ggctcgcggc ctggcaagaa tgtacagctg acagagaacg agatccgcgg tctgtgcctg 120
aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag 180
atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt 240
ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc 300
ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg 360
ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc 420
aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc 480
atcgcggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg 540
cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg 600
ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac 660
cgtggcgtct cttttacctt tggagccgag gtggtggcca agttcctcca caagcacgac 720
ttggacctca tctgccgagc acaccaggtg gtagaagacg gctacgagtt ctttgccaag 780
cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc 840
gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac 900
aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc 960
ccaccccgca attccgccaa agccaagaaa tag   993

<210> 15
<211> 330
<212> PRT
<213> Homo sapiens

<400> 15
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Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
 1               5                  10                  15
Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
            20                  25                  30
Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35                  40                  45
Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50                  55                  60
Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65                  70                  75                  80
Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85                  90                  95
Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100                 105                 110
Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115                 120                 125
Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130                 135                 140
```

```
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205
Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285
Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
    290                 295                 300
Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305                 310                 315                 320
Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
                325                 330
```

<210> 16
<211> 702
<212> DNA
<213> Murinae

<400> 16
ggcatgacag gcagtgagca ggtgatgagc caggttgtgg atctctttag tgagggaata 60
ggctgctgga gatatggctg tggtctacaa ggaggctggg gaactagcaa ggagatgctc 120
tctcagctat cacagcctta cagcaaagcc actatctctt tggattttga aattttctct 180
gccatgccta tgactatttt aaaattgggc aaagtatatc catttcagag gggctttttc 240
tgtactgaca acagcgtgaa gtacccgtac catgacagta ccatcccgtc ccgtatactc 300
gccatactgg ggcttggctt acccattttc tctatgagta tggagaatct ctgtctgttt 360
actttaatgt cttgcattcg aattcctttg tcggcaatcc ctacatagcc accatttaca 420
aagccgtcgg agccttttgt tcggagtctc agctagtcag tccttgactg acatcgctaa 480
gtatactata ggcagtttgc ggccgcactt cttggctatc tgtaacccag actggtcaaa 540
aatcaactgc agtgatggct atattgagga ctacatatgt caagggaatg aagagaaagt 600
caaggagggc aggttgtctt tctactcggg acactcttca ttctctatgt actgcatgct 660
gtttgtcgca ctttatcttc aagccaggat gaagggagac tg 702

<210> 17
<211> 1432
<212> DNA
<213> Murinae

<400> 17
catccttaga gctcgcccgg cctgttggag agggcacagg gcagcggagg gcgattggcc 60
gcgacgagcc agcactgaga gagcaggcgc ctgaggcgac agatcggcgg ccactcggtg 120
gcagggcggc ccaatccaaa ctgccctggt ccctgctccc gtcagtctaa gaggctcgca 180
gtcgcttggg gcggccgcca tcccgagggc ggggctctgg gaattgggta tctggaccgc 240

```
cgcggtctgt tcctcccgcc actcgcacca ggtggtgaca ccatccagcc ggtgaccatg 300
ttcgacaaga cgcggctgcc gtacgtggcc ctcgatgtga tttgcgtgtt gctggctgga 360
ttgccttttg caattcttac ttcaaggcat acccccttcc agcgaggaat attctgtaat 420
gatgactcca tcaagtaccc ttacaaggaa gacaccatac cttatgcctt attaggtgga 480
atagtcattc cattctgtat tatcgttatg agtattggag aatctctgtc tgtttacttt 540
aatgtcttgc attcgaattc ctttgtcggc aatccctaca tagccaccat ttacaaagcc 600
gtcggagcct ttttgttcgg agtctcagct agtcagtcct tgactgacat cgctaagtat 660
actataggca gtttgcggcc gcacttcttg gctatctgta acccagactg gtcaaaaatc 720
aactgcagtg atggctatat tgaggactac atatgtcaag ggaatgaaga gaaagtcaag 780
gagggcaggt tgtctttcta ctcgggacac tcttcattct ctatgtactg catgctgttt 840
gtcgcacttt atcttcaagc caggatgaag ggagactggg caagactctt acgacccatg 900
ctccagtttg ggctcattgc tttttccata tatgtgggcc tttctcgagt gtctgactac 960
aaacaccact ggagtgacgt cacagttgga ctcattcagg gagctgctat ggctatactg 1020
gttgctttgt atgtatccga tttcttcaag gacacacatt cttacaaaga gagaaaggaa 1080
gaggatccac acacgactct ccatgaaacc gccagttcac ggaactactg ggcgctggcc 1140
cgcttcaaag gcaacagctg gaggctaaag gcaggggat gcgtattact tcctgctgta 1200
cagaccattc tataaaggac tgctgctatc tatacctcct ggatgcccat tttatgtgtg 1260
tacagttact tctaacacaa tgagtaacag ttcaattaaa gaaaatgaag cctgtcacta 1320
aaacactgtc ccacctgtac atttttattg aaagacgcta tgtacaaatg tgtatgttac 1380
atgccttctc agaatgatgt tgacttaaat ataataaaaa gcttgtgaac ca          1432
```

<210> 18
<211> 378
<212> PRT
<213> Murinae

<400> 18

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Glu Ser Arg Arg Leu Arg Arg Gln Ile Gly Gly His Ser Val Ala Gly
 1               5                  10                  15
Arg Pro Asn Pro Asn Cys Pro Gly Pro Cys Ser Arg Gln Ser Lys Arg
            20                  25                  30
Leu Ala Val Ala Trp Gly Gly Arg His Pro Glu Gly Gly Ala Leu Gly
        35                  40                  45
Ile Gly Tyr Leu Asp Arg Arg Gly Leu Phe Leu Pro Pro Leu Ala Pro
    50                  55                  60
Gly Gly Asp Thr Ile Gln Pro Val Thr Met Phe Asp Lys Thr Arg Leu
65                  70                  75                  80
Pro Tyr Val Ala Leu Asp Val Ile Cys Val Leu Leu Ala Gly Leu Pro
                85                  90                  95
Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg Gly Ile Phe
            100                 105                 110
Cys Asn Asp Asp Ser Ile Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro
        115                 120                 125
Tyr Ala Leu Leu Gly Gly Ile Val Ile Pro Phe Cys Ile Ile Val Met
    130                 135                 140
Ser Ile Gly Glu Ser Leu Ser Val Tyr Phe Asn Val Leu His Ser Asn
145                 150                 155                 160
Ser Phe Val Gly Asn Pro Tyr Ile Ala Thr Ile Tyr Lys Ala Val Gly
                165                 170                 175
Ala Phe Leu Phe Gly Val Ser Ala Ser Gln Ser Leu Thr Asp Ile Ala
            180                 185                 190
Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu Ala Ile Cys Asn
        195                 200                 205
Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Asp Tyr
    210                 215                 220
```

```
Ile Cys Gln Gly Asn Glu Glu Lys Val Lys Glu Gly Arg Leu Ser Phe
225                 230                 235                 240
Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala
                245                 250                 255
Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg
            260                 265                 270
Pro Met Leu Gln Phe Gly Leu Ile Ala Phe Ser Ile Tyr Val Gly Leu
        275                 280                 285
Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Thr Val Gly
    290                 295                 300
Leu Ile Gln Gly Ala Ala Met Ala Ile Leu Val Ala Leu Tyr Val Ser
305                 310                 315                 320
Asp Phe Phe Lys Asp Thr His Ser Tyr Lys Glu Arg Lys Glu Glu Asp
                325                 330                 335
Pro His Thr Thr Leu His Glu Thr Ala Ser Ser Arg Asn Tyr Trp Ala
            340                 345                 350
Leu Ala Arg Phe Lys Gly Asn Ser Trp Arg Leu Lys Ala Gly Gly Cys
        355                 360                 365
Val Leu Leu Pro Ala Val Gln Thr Ile Leu
    370                 375
```

<210> 19
<211> 1626
<212> DNA
<213> Homo sapiens

<400> 19
tcagcgggag gggctggacc ccgcgttcct cctccctgcc ggtccccatc cttaaagcga 60
gagtctggac gccccgcctg tgggagagag cgccgggatc cggacgggga gcaaccgggg 120
caggccgtgc cggctgagga ggtcctgagg ctacagagct gccgcggctg gcacacgagc 180
gcctcggcac taaccgagtg ttcgcggggg ctgtgagggg agggccccgg gcgccattgc 240
tggcggtggg agcgccgccc ggtctcagcc cgccctcggc tgctctcctc ctccggctgg 300
gaggggccgt agctcggggc cgtcgccagc cccggccccgg gctcgagaat caagggcctc 360
ggccgccgtc ccgcagctca gtccatcgcc cttgccgggc agcccgggca gagaccatgt 420
ttgacaagac gcggctgccg tacgtggccc tcgatgtgct ctgcgtgttg ctggcttcca 480
tgcctatggc tgttctaaaa ttgggccaaa tatatccatt tcagagaggc tttttctgta 540
aagacaacag catcaactat ccgtaccatg acagtaccgt cacatccact gtcctcatcc 600
tagtgggggt tggcttgccc atttcctcta ttattcttgg agaaaccctg tctgtttact 660
gtaacctttt gcactcaaat tcctttatca ggaataacta catagccact atttacaaag 720
ccattggaac ctttttattt ggtgcagctg ctagtcagtc cctgactgac attgccaagt 780
attcaatagg cagactgcgg cctcacttct tggatgtttg tgatccagat tggtcaaaaa 840
tcaactgcag cgatggttac attgaatact acatatgtcg agggaatgca gaaagagtta 900
aggaaggcag gttgtccttc tattcaggcc actcttcgtt ttccatgtac tgcatgctgt 960
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cactgcaatt tggtcttgtt gccgtatcca tttatgtggg cctttctcga gtttctgatt 1080
ataaacacca ctggagcgat gtgttgactg gactcattca gggagctctg gttgcaatat 1140
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aggaggactc tcatacaact ctgcatgaaa caccaacaac tgggaatcac tatccgagca 1260
atcaccagcc ttgaaaggca gcagggtgcc caggtgaagc tggcctgttt tctaaaggaa 1320
aatgattgcc acaaggcaag aggatgcatc tttcttcctg gtgtacaagc ctttaaagac 1380
ttctgctgct gctatgcctc ttggatgcac actttgtgtg tacatagtta cctttaactc 1440
agtggttatc taatagctct aaactcatta aaaaaactcc aagccttcca ccaaaacagt 1500
gccccacctg tatacatttt tattaaaaaa atgtaatgct tatgtataaa catgtatgta 1560
atatgctttc tatgaatgat gtttgattta aatataatac atattaaaat gtatgggaga 1620

accaaa 1626

<210> 20
<211> 378
<212> PRT
<213> Homo sapiens

<400> 20
Gly Gly Pro Glu Ala Thr Glu Leu Pro Arg Leu Ala His Glu Arg Leu
 1   5   10   15
Gly Thr Asn Arg Val Phe Ala Gly Ala Val Arg Gly Gly Pro Arg Ala
            20   25   30
Pro Leu Leu Ala Val Gly Ala Pro Pro Gly Leu Ser Pro Pro Ser Ala
        35   40   45
Ala Leu Leu Leu Arg Leu Gly Gly Ala Val Ala Arg Gly Arg Arg Gln
    50   55   60
Pro Arg Pro Gly Leu Glu Asn Gln Gly Pro Arg Pro Pro Ser Arg Ser
65   70   75   80
Ser Val His Arg Pro Cys Arg Ala Ala Arg Ala Glu Thr Met Phe Asp
                85   90   95
Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu
            100   105   110
Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe
        115   120   125
Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His
    130   135   140
Asp Ser Thr Val Thr Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu
145   150   155   160
Pro Ile Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn
                165   170   175
Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile
            180   185   190
Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser
        195   200   205
Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe
    210   215   220
Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly
225   230   235   240
Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu
                245   250   255
Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys
            260   265   270
Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp
        275   280   285
Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser
    290   295   300
Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser
305   310   315   320
Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val
                325   330   335
Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu
            340   345   350
Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr
        355   360   365
Gly Asn His Tyr Pro Ser Asn His Gln Pro

370 375

<210> 21
<211> 816
<212> DNA
<213> Homo sapiens

<400> 21
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ttccaacgag gagtattctg taatgatgag tccatcaagt acccttacaa agaagacacc 120
ataccttatg cgttattagg tggaataatc attccattca gtattatcgt tattattctt 180
ggagaaaccc tgtctgttta ctgtaacctt ttgcactcaa attcctttat caggaataac 240
tacatagcca ctatttacaa agccattgga acctttttat ttggtgcagc tgctagtcag 300
tccctgactg acattgccaa gtattcaata ggcagactgc ggcctcactt cttggatgtt 360
tgtgatccag attggtcaaa aatcaactgc agcgatggtt acattgaata ctacatatgt 420
cgagggaatg cagaaagagt taaggaaggc aggttgtcct tctattcagg ccactcttcg 480
ttttccatgt actgcatgct gtttgtggca ctttatcttc aagccaggat gaagggagac 540
tgggcaagac tcttacgccc cacactgcaa tttggtcttg ttgccgtatc catttatgtg 600
ggcctttctc gagtttctga ttataaacac cactggagcg atgtgttgac tggactcatt 660
cagggagctc tggttgcaat attagttgct gtatatgtat cggatttctt caaagaaaga 720
acttctttta aagaaagaaa agaggaggac tctcatacaa ctctgcatga aacaccaaca 780
actgggaatc actatccgag caatcaccag ccttga 816

<210> 22
<211> 271
<212> PRT
<213> Homo sapiens

<400> 22
Ile Tyr Ser Leu Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser
1 5 10 15
Arg His Thr Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile
20 25 30
Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly
35 40 45
Ile Ile Ile Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu
50 55 60
Ser Val Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn
65 70 75 80
Tyr Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala
85 90 95
Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg
100 105 110
Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile
115 120 125
Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala
130 135 140
Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser
145 150 155 160
Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg
165 170 175
Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly
180 185 190
Leu Val Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr

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        195                 200                 205
Lys His His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu
    210                 215                 220
Val Ala Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg
225                 230                 235                 240
Thr Ser Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His
                245                 250                 255
Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
            260                 265                 270
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<210> 23
<211> 840
<212> DNA
<213> Murinae

<220>
<221> misc_feature
<222> 474
<223> n is a, c, g, or t

<400> 23
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agtacagggg cctggtgcgc aaagggaaga aaagcaaaag acgaaaatgg ctaaatttaa 180
gatccgtcca gccactgcct ctgactgcag tgacatcctg cgactgatca aggaactggc 240
taaatatgaa tacatggaag atcaagtcat tttaactgag aaagatctcc aagaggatgg 300
ctttggagaa cacccttct accactgcct ggttgcagaa gtgcctaaag agcactggac 360
ccctgaagga catagcattg ttgggttcgc catgtactat tttacctatg acccatggat 420
tggcaagttg ctgtatcttg aagacttctt cgtgatgagt gattacagag gctntggtat 480
aggatcagaa attttgaaga atctaagcca ggttgccatg aagtgtcgct gcagcagtat 540
gcacttcttg gtagcagaat ggaatgaacc atctatcaac ttctacaaaa gaagaggtgc 600
ttcggatctg tccagtgaag agggatggga ggctcttcaa gattgacaag agtacttgct 660
aaaaatggca gcagaggagt gaggcgtgcc ggtgtagaac atgacaacct ccattgtgct 720
ttagaataat tctcagcttc ccttgctttc tatcttgtgg tgtaggtgaa ataatagagc 780
gagccaccat tccaaagctt tattaccagt gacgtgttgc atgtttgaaa tcggtctggt 840

<210> 24
<211> 1052
<212> DNA
<213> Murinae

<400> 24
gctgcgcagt ttccccgaag taagtttgcc agttttctgt cttatactga ggttcgccgg 60
gtcatggtgc cagcctgact gagaagagga cgctcccggg aaacgaatga ggaaccacct 120
cctcctgctg ttcaagtaca ggggcctggt gcgcaaaggg aagaaaagca aaagacgaaa 180
atggctaaat ttaagatccg tccagccact gcctctgact gcagtgacat cctgcgactg 240
atcaaggaac tggctaaata tgaatacatg gaagatcaag tcattttaac tgagaaagat 300
ctccaagagg atggctttgg agaacacccc ttctaccact gcctggttgc agaagtgcct 360
aaagagcact ggacccctga aggacatagc attgttgggt tcgccatgta ctattttacc 420
tatgacccat ggattggcaa gttgctgtat cttgaagact tcttcgtgat gagtgattac 480
agaggctttg gtataggatc agaaattttg aagaatctaa gccaggttgc catgaagtgt 540
cgctgcagca gtatgcactt cttggtagca gaatggaatg aaccatctat caacttctac 600
aaaagaagag gtgcttcgga tctgtccagt gaagagggat ggaggctctt caagattgac 660

aaagagtact tgctaaaaat ggcagcagag gagtgaggcg tgccggtgta gacaatgaca 720
acctccattg tgctttagaa taattctcag cttcccttgc tttctatctt gtgtgtagtg 780
aaataataga gcgagcaccc attccaaagc tttattacca gtgacgttgt tgcatgtttg 840
aaattcggtc tgtttaaagt ggcagtcatg tatgtggttt ggaggcagaa ttcttgaaca 900
tcttttgatg aagaacaagg tggtatgatc ttactatata agaaaaacaa aacttcattc 960
ttgtgagtca tttaaatgtg tacaatgtac acactggtac ttagagtttc tgttttgatt 1020
ctttttttt taaataaact actctttgat tt 1052

<210> 25
<211> 171
<212> PRT
<213> Murinae

<400> 25
Met Ala Lys Phe Lys Ile Arg Pro Ala Thr Ala Ser Asp Cys Ser Asp
 1   5   10   15
Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met Glu Asp
            20   25   30
Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu
        35   40   45
His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp
    50   55   60
Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr
65   70   75   80
Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val
                85   90   95
Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn
            100   105   110
Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu
        115   120   125
Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly
    130   135   140
Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp
145   150   155   160
Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu
                165   170

<210> 26
<211> 1111
<212> DNA
<213> Homo sapiens

<400> 26
gcgcagctct tagtcgcggg ccgactggtg tttatccgtc actcgccgag gttccttggg 60
tcatggtgcc agcctgactg agaagaggac gctcccggga gacgaatgag gaaccacctc 120
ctcctactgt tcaagtacag gggcctggtc cgcaaaggga agaaaagcaa aagacgaaaa 180
tggctaaatt cgtgatccgc ccagccactg ccgccgactg cagtgacata ctgcggctga 240
tcaaggagct ggctaaatat gaatacatgg aagaacaagt aatcttaact gaaaaagatc 300
tgctagaaga tggttttgga gagcacccct tttaccactg cctggttgca gaagtgccga 360
aagagcactg gactccggaa ggtaacccct cgccctttcc agaagccaga gagaccaaca 420
ttgttggttt tgccatgtac tattttacct atgacccgtg gattggcaag ttattgtatc 480
ttgaggactt cttcgtgatg agtgattata gaggtacgat tgagctttgg cataggatca 540
gaaattctga agaatctaag ccaggttgca atgaggtgtc gctggcagca tgcacttctt 600
gggcagaatg gaatgaacca tccatcaact tctataaaag aagaggtgct tctgatctgt 660

ccagtgaaga gggttggaga ctgttcaaga tcgacaagga gtacttgcta aaaatggcaa 720
cagaggagtg aggagtgctg ctgtagatga caacctccat tctattttag aataaattcc 780
caacttctct tgctttctat gctgtttgta gtgaaataat agaatgagca cccattccaa 840
agctttatta ccagtggcgt tgttgcatgt ttgaaatgag gtctgtttaa agtggcaatc 900
tcagatgcag tttggagagt cagatctttc tccttgaata tctttcgata aacaacaagg 960
tggtgtgatc ttaatatatt tgaaaaaaac ttcattctcg tgagtcattt aaatgtgtac 1020
aatgtacaca ctggtactta gagtttctgt ttgattcttt tttaataaac tactctttga 1080
tttaattcta aaaaaaaaaa aaaaaaagac a 1111

<210> 27
<211> 190
<212> PRT
<213> Homo sapiens

<400> 27
Glu Pro Pro Pro Pro Thr Val Gln Val Gln Gly Pro Gly Pro Gln Arg
 1   5   10   15
Glu Glu Lys Gln Lys Thr Lys Met Ala Lys Phe Val Ile Arg Pro Ala
            20   25   30
Thr Ala Ala Asp Cys Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu Ala
        35   40   45
Lys Tyr Glu Tyr Met Glu Glu Gln Val Ile Leu Thr Glu Lys Asp Leu
    50   55   60
Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Val Ala
65   70   75   80
Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly Asn Pro Ser Pro Phe
                85   90   95
Pro Glu Ala Arg Glu Thr Asn Ile Val Gly Phe Ala Met Tyr Tyr Phe
            100   105   110
Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe
        115   120   125
Val Met Ser Asp Tyr Arg Gly Thr Ile Glu Leu Trp His Arg Ile Arg
    130   135   140
Asn Ser Glu Glu Ser Lys Pro Gly Cys Asn Glu Val Ser Leu Ala Ala
145   150   155   160
Cys Thr Ser Trp Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys
                165   170   175
Arg Arg Gly Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg
            180   185   190

<210> 28
<211> 745
<212> DNA
<213> Murinae

<400> 28
aatctatgga gcagattcgg cgaattatga gaccaactga tgtaccagat caaggtcttc 60
tttgtgatct ttggtggtct gaccccgatg aaagatgtct taggctgggg tgaaaatgac 120
agaggagtgt ccttcacatt tggtgcagaa gtggttgcaa aatttctcca taagcatgat 180
tcggatctta tatgtagagc ccatcaggtg gttgaagatg gctatgagtt tttcgcaaag 240
aggcagttag tcactctgtt gttctgcgag cccaactact gtggcgagtt tgacaatgca 300
ggcgccatga tgagtgtgga tgagaccctc atgtgttcct tccagatttt aaagcctgca 360
gagaaaaaga agcccaacgc cacgagacct gtcacaccac cacggggtat gatcacaaag 420
caagcaaaga aatagatgtc acttgacact gcctggttgg gacttgtaac atagcgttca 480

taaccttcct ttttaaactg tgatgtgctg gtcagcttgc ccaggtagac ctgtctgtcg 540
ggccctcctc catttgatta ctgctggcac ttgctggtta tagcagcaag ccaagcactt 600
cattctcaag agagcatttg gttctgaacc tctgttccct ttgtggacag ctctgatgat 660
ggtgttaagc tgtacaccct ggcaggttat cctgtctgag gagaaagtgt acaattgatc 720
ttttttagt ttagtataag tcatg 745

<210> 29
<211> 2127
<212> DNA
<213> Murinae

<400> 29
gctgctgcgg gagggtcggc ggcgggacgg cgatggcgga tatcgacaaa ctcaacatcg 60
acagcatcat ccaacggctg ctggaagtga gagggtccaa gccaggcaag aatgtccagc 120
tccaggagaa cgagatccga ggactctgcc tgaagtctcg ggagatcttc ctcagtcagc 180
ctatcctttt agaacttgaa gcaccactca agatatgtgg tgacatccac gggcagtact 240
atgatttgct ccgtctgttt gaatacggtg gctttcctcc agagagcaac tatttgtttc 300
tcggggacta tgtggacagg ggcaagcagt ccctggagac aatctgcctc ttgctggcct 360
acaaaatcaa gtatccggag aacttctttc ttctcagagg gaaccacgag tgcgccagca 420
tcaataggat ctacggattt tatgatgagt gtaaaagaag atacaacatt aagctgtgga 480
aaacgttcac agactgtttt aactgcttgc cgatagcagc catcgtggac gagaagatat 540
tctgctgtca tggaggttta tcaccagatc ttcaatctat ggagcagatt cggcgaatta 600
tgagaccaac tgatgtacca gatcaaggtc ttctttgtga tcttttgtgg tctgaccccg 660
ataaagatgt cttaggctgg ggtgaaaatg acagaggagt gtccttcaca tttggtgcag 720
aagtggttgc aaaatttctc cataagcatg atttggatct tatatgtaga gcccatcagg 780
tggttgaaga tggctatgag ttttttgcaa agaggcagtt agtcactctg ttttctgcac 840
ccaactactg tggcgagttt gacaatgcag gcgccatgat gagtgtggat gagaccctca 900
tgtgttcctt ccagatttta aagcctgcag agaaaaagaa gcccaacgcc acgagacctg 960
tcacaccacc acggggtatg atcacaaagc aagcaaagaa atagatgtca cttgacactg 1020
cctggttggg acttgtaaca tagcgttcat aaccttcctt tttaaactgt gatgtgctgg 1080
tcagcttgcc caggtagacc tgtctgtcgg gccctcctcc atttgattac tgctggcact 1140
tgctggttat agcagcaagc caagcacttc attctcaaga gagcattttg ttttgaacct 1200
ctgttccctt tgtggacagc tctgatgatg gtgttaagct gtacaccctg gcaggttatc 1260
ctgtctgagg agaaagtgta caattgatct ttttttaatt tagtataagt catgaataat 1320
gtaaatgcct gttttcttta ggatataaag agagccttag agtgcgtgag tctctacatg 1380
taattgtcat aaatgcattc tgttgataca aaccactgtg aacaattttt tttccagttt 1440
gtttgaaagg gactgctttc cctcattgtc ttgtcatgta caaactagtg tctgcagctg 1500
tggcagcagg agtgacctgc ctgccgccag ccctgcccag actatctgaa gcacactcct 1560
tcccactgca catttaataa tgattaaagc cattcttttc aatgtctgtg attccttcct 1620
aaagccaaag tttctgttgg actgtatggc acgccctggg gatgaggtgg ccagggcatc 1680
gaggctgcgt gcacaggccg cctccctccg tggggcctca gaagcaggtt attttaacta 1740
gcaatagtgg tatagtgctg agtaagctat taatgatgga agttaatgac actttgtaca 1800
gttcccatat agtctattca ctgagtgatc tttttacagt tggatcaggc ctgaacccgt 1860
ccattcagaa agcttcaaat tatagaaaca acactgtcct atacgagtga ccgataatgc 1920
tttctttggc tacattcttt attctgcggt gacattgagg cttataaatc aaaaggaact 1980
aacttgccgt ccaccggttt atacagaact cacagtatct atgacttttt taaactacga 2040
cctgttaaat gaatctgttt gcacagatgc ccgtgtacaa tgccatgtgc tgagaatggt 2100
ttcagactta ttaaatgcaa gcttgtt 2127

<210> 30
<211> 323
<212> PRT
<213> Murinae

<400> 30

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Met Ala Asp Ile Asp Lys Leu Asn Ile Asp Ser Ile Ile Gln Arg Leu
 1               5                  10                  15
Leu Glu Val Arg Gly Ser Lys Pro Gly Lys Asn Val Gln Leu Gln Glu
            20                  25                  30
Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35                  40                  45
Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50                  55                  60
Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65                  70                  75                  80
Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85                  90                  95
Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100                 105                 110
Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115                 120                 125
Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130                 135                 140
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205
Pro Asp Lys Asp Val Leu Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285
Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Glu Lys Lys Lys Pro
    290                 295                 300
Asn Ala Thr Arg Pro Val Thr Pro Pro Arg Gly Met Ile Thr Lys Gln
305                 310                 315                 320
Ala Lys Lys
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<210> 31
<211> 993
<212> DNA
<213> Homo sapiens

<400> 31
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ggctcgcggc ctggcaagaa tgtacagctg acagagaacg agatccgcgg tctgtgcctg 120
aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag 180
atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt 240
ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc 300

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ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg 360
ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc 420
aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc 480
atcgcggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg 540
cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg 600
ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac 660
cgtggcgtct cttttacctt tggagccgag gtggtggcca agttcctcca caagcacgac 720
ttggacctca tctgccgagc acaccaggtg gtagaagacg gctacgagtt ctttgccaag 780
cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc 840
gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac 900
aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc 960
ccaccccgca attccgccaa agccaagaaa tag                               993

<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

<400> 32
Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
 1               5                  10                  15
Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
            20                  25                  30
Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35                  40                  45
Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50                  55                  60
Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65                  70                  75                  80
Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85                  90                  95
Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100                 105                 110
Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115                 120                 125
Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130                 135                 140
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205
Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285
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Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
    290                 295                 300
Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305                 310                 315                 320
Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
                325                 330
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<210> 33
<211> 747
<212> DNA
<213> Murinae

<220>
<221> misc_feature
<222> 298
<223> n is a, c, g, or t

<400> 33
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ttcgttggcc tgtatgacct ggacgcctct cgctacttcg tccttctgcc tctgtgcctc 120
tgcgtatttg ttgagctggg agagtagccc agtggtacag cgcccacctg gaatacttga 180
ggacctgggg ttgtctccca gcactgcaaa aggaaaattc actgttacag tcttccttgc 240
acttaaacca gctttgtcta ttgtttttt ggtttggctt tgttactttt gttgctgntt 300
atttttgttg ttgttgtttg tttgtttgag acagggtttt tttgctagcc ctgactgtcc 360
tgaaactccc tctgtagacc aggctggcct caaacttaca gagatccgcc tgcctcagcc 420
tcccaagtgc tgggaataat ggtgtggtca ccaccgccca gccttttgtc tatttttaaa 480
cttgaaagaa acaacagccc agatttcaaa aataatataa tgcacttata cctaaaaaaa 540
caaccaggag tgcccagtta ataacatttt ttaaatgtgg ggatgggaag ggcattagag 600
gagtcttcct tctattgaag attcattaaa gtatttaaga tatgcccttt cactctttat 660
ataaatccaa gatttttctt tgctgaagta tttaaaactt ttgtaccttt atatgtagat 720
atgaatttga aaatatgctt atgtgta   747

<210> 34
<211> 2021
<212> DNA
<213> Murinae

<400> 34
gggcaagaaa cttcaacaga agtccacacc tccccagaag catccgtcaa agagggacga 60
gcagaccgag caaacactcc cagcgccaaa gatcgggact gtggggaatc tgcagggccc 120
agttccaagc tctctgggaa ccggaacggc agggaaagcc gagcgggcgg cctgaaggag 180
agaagcaatg gatcagaggg ggctccaagt gaaggaaggg taagtccaaa gagcagcgtt 240
cctgagactg gcctgataga ctgcagcact tcacaggccg ccagttctcc agaaccaacc 300
agcctcaagg gctccacatc tctgcctgtt cactcagctt ccagagctag gaaagagcag 360
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gtagaccagg ctggcctcaa acttacagag atctgcctgc ctcagcctcc cgagtgctgg 780
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ccagttaata acacttttta aatgtgggga tgggaagggc attagaggag tcttccttct 960

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gttttcttag atactttgat cccattggag ctctgttaaa gtttaaaatg aaaattatca 1920
tgtactgtat gggaaatgta aatactaact tttccacata tgtaaacttc agacacaaat 1980
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<210> 35
<211> 709
<212> PRT
<213> Murinae

<400> 35
Met Glu Arg Ser Pro Phe Leu Leu Ala Cys Ile Leu Leu Pro Leu Val
 1   5   10   15
Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
            20   25   30
Met Lys Met Thr Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
        35   40   45
Tyr Asp Gln Gly Ile Ala Ala Val Glu Met Gly His Phe Leu His Leu
    50   55   60
Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Met Phe Leu Cys Gln Ala
65   70   75   80
Phe Ile Pro Thr Cys Thr Glu Gln Ile His Val Val Leu Pro Cys Arg
                85   90   95
Lys Leu Cys Glu Lys Ile Val Ser Asp Cys Lys Lys Leu Met Asp Thr
            100   105   110
Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asn Arg Leu Pro His
        115   120   125
Cys Asp Asp Thr Val Pro Val Thr Ser His Pro His Thr Glu Leu Ser
    130   135   140
Gly Pro Gln Lys Lys Ser Asp Gln Val Pro Arg Asp Ile Gly Phe Trp
145   150   155   160
Cys Pro Lys His Leu Arg Thr Ser Gly Asp Gln Gly Tyr Arg Phe Leu
                165   170   175
Gly Ile Glu Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
            180   185   190
Asp Glu Leu Asp Phe Ala Lys Ser Phe Ile Gly Ile Val Ser Ile Phe
        195   200   205
Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
    210   215   220
Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225   230   235   240

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Tyr Ser Ile Val Ser Leu Met Tyr Phe Val Gly Phe Leu Leu Gly Asn
                245                 250                 255
Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
            260                 265                 270
Val Val Leu Gly Ser Lys Asn Lys Ala Cys Ser Val Val Phe Met Phe
        275                 280                 285
Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
    290                 295                 300
Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305                 310                 315                 320
Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Ala Pro Gly
                325                 330                 335
Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
            340                 345                 350
Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
        355                 360                 365
Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
    370                 375                 380
Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385                 390                 395                 400
Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
                405                 410                 415
Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
            420                 425                 430
Gly Cys Tyr Val Tyr Glu Leu Val Asn Arg Ile Thr Trp Glu Met Thr
        435                 440                 445
Trp Phe Ser Asp His Cys His Gln Tyr Arg Ile Pro Cys Pro Tyr Gln
    450                 455                 460
Ala Asn Pro Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465                 470                 475                 480
Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
                485                 490                 495
Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
            500                 505                 510
Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
        515                 520                 525
Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Gly
    530                 535                 540
Ala Pro Gly Pro His Arg Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545                 550                 555                 560
Ser Thr Gly Ala Thr Thr Asn His Gly Thr Ser Ala Met Ala Ile Ala
                565                 570                 575
Asp His Asp Tyr Leu Gly Gln Glu Thr Ser Thr Glu Val His Thr Ser
            580                 585                 590
Pro Glu Ala Ser Val Lys Glu Gly Arg Ala Asp Arg Ala Asn Thr Pro
        595                 600                 605
Ser Ala Lys Asp Arg Asp Cys Gly Glu Ser Ala Gly Pro Ser Ser Lys
    610                 615                 620
Leu Ser Gly Asn Arg Asn Gly Arg Glu Ser Arg Ala Gly Gly Leu Lys
625                 630                 635                 640
Glu Arg Ser Asn Gly Ser Glu Gly Ala Pro Ser Glu Gly Arg Val Ser
                645                 650                 655
Pro Lys Ser Ser Val Pro Glu Thr Gly Leu Ile Asp Cys Ser Thr Ser
            660                 665                 670
Gln Ala Ala Ser Ser Pro Glu Pro Thr Ser Leu Lys Gly Ser Thr Ser
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675 680 685
Leu Pro Val His Ser Ala Ser Arg Ala Arg Lys Glu Gln Gly Ala Gly
690 695 700
Ser His Ser Asp Ala
705

<210> 36
<211> 2039
<212> DNA
<213> Homo sapiens

<400> 36
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cattatttcc ttaaatcatg ttcgacaagt catacaacat gatggccgga accaagaaaa 180
actaaagaaa tttatgattc gaattggagt cttcagcggc ttgtatcttg tgccattagt 240
gacacttctc ggatgttacg tctatgagca agtgaacagg attacctggg agataacttg 300
ggtctctgat cattgtcgtc agtaccatat cccatgtcct tatcaggcaa aagcaaaagc 360
tcgaccagaa ttggctttat ttatgataaa atacctgatg acattaattg ttggcatctc 420
tgctgtcttc tgggttggaa gcaaaaagac atgcacagaa tgggctgggt tttttaaacg 480
aaatcgcaag agagatccaa tcagtgaaag tcgaagagta ctacaggaat catgtgagtt 540
tttcttaaag cacaattcta aagttaaaca caaaaagaag cactataaac caagttcaca 600
caagctgaag gtcatttcca aatccatggg aaccagcaca ggagctacag caaatcatgg 660
cacttctgca gtagcaatta ctagccatga ttacctagga caagaaactt tgacagaaat 720
ccaaacctca ccagaaacat caatgagaga ggtgaaagcg gacggagcta gcacccccag 780
gttaagagaa caggactgtg gtgaacctgc ctcgccagca gcatccatct ccagactctc 840
tggggaacag gtcgacggga agggccaggc aggcagtgta tctgaaagtg cgcggagtga 900
aggaaggatt agtccaaaga gtgatattac tgacactggc ctggcacaga gcaacaattt 960
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cccggtttca ggagtgagaa aagagcaggg aggtggttgt cattcagata cttgaagaac 1080
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ctggaaaaaa tagagttcaa gaataatatg actcatttca cacaaaggtt aatgacaaca 1260
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aagatgtact atgctatttt actttttga tataaaatca agatatttct ttgctgaagt 1440
atttaaatct tatccttgta tctttttata catatttgaa aataagctta tatgtatttg 1500
aacttttttg aaatcctatt caagtatttt tatcatgcta ttgtgatatt ttagcacttt 1560
ggtagctttt acactgaatt tctaagaaaa ttgtaaaata gtcttctttt atactgtaaa 1620
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ccttaccatc taaaatgtgt gatttttata gtctcgtttt aggaatttca cagatctaaa 1740
ttatgtaact gaaataaggt gcttactcaa agagtgtcca ctattgattg tattatgctg 1800
ctcactgatc cttctgcata tttaaaataa aatgtcctaa agggttagta gacaaaatgt 1860
tagtcttttg tatattaggc caagtgcaat tgacttccct tttttaatgt ttcatgacca 1920
cccattgatt gtattataac cacttacagt tgcttatatt ttttgtttta acttttgttt 1980
tttaacattt agaatattac attttgtatt atacagtacc tttctcagac attttgtag 2039

<210> 37
<211> 706
<212> PRT
<213> Homo sapiens

<400> 37
Met Glu Met Phe Thr Phe Leu Leu Thr Cys Ile Phe Leu Pro Leu Leu

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            20                  25                  30
Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
        35                  40                  45
Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
    50                  55                  60
Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65                  70                  75                  80
Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
                85                  90                  95
Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
            100                 105                 110
Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
        115                 120                 125
Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
    130                 135                 140
Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145                 150                 155                 160
Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
                165                 170                 175
Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
            180                 185                 190
Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe
        195                 200                 205
Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
    210                 215                 220
Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225                 230                 235                 240
Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp
                245                 250                 255
Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
            260                 265                 270
Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu
        275                 280                 285
Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
    290                 295                 300
Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305                 310                 315                 320
Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly
                325                 330                 335
Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
            340                 345                 350
Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
        355                 360                 365
Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
    370                 375                 380
Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385                 390                 395                 400
Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
                405                 410                 415
Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
            420                 425                 430
Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr
        435                 440                 445
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Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln
    450                 455                 460
Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465                 470                 475                 480
Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
                485                 490                 495
Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
            500                 505                 510
Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
        515                 520                 525
Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr
    530                 535                 540
Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545                 550                 555                 560
Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr
                565                 570                 575
Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser
            580                 585                 590
Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro
        595                 600                 605
Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser
    610                 615                 620
Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly
625                 630                 635                 640
Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser
                645                 650                 655
Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro
            660                 665                 670
Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val
        675                 680                 685
His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Gly Cys His Ser
    690                 695                 700
Asp Thr
705
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<210> 38
<211> 773
<212> DNA
<213> Murinae

<400> 38
ctgaggtgct agcaccagcc tggttgtctc tggcgggcct gaagcaagca tggatcaaga 60
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gttctttgcc cacaaggtgg agcatgaaag caaggcgcat aatgggagaa gcttccagag 180
gaccgggact cttgcctttg agcgggtcta cactgccaac cagaactgcg tagatgcgta 240
ccccactttc cttgtggtac tctggactgc aggactactt tgcagccaag tccctgcagc 300
cttcgccgga ctgatgtacc tgtttgtgag gcaaaaatac tttgtcggct atctgggaga 360
gagaactcag agcacccctg gctacatctt cggcaagcgg atcatcctgt tcctgttcct 420
catgtccttc gccgggatac tcaaccatta cctcatcttc ttcttcggaa gcgactttga 480
gaactacatc agaacggtaa gcacgacgat ctccccgctg cttctcatcc cctgattgct 540
ggagacagag aaggacgctc accagatcaa tagagacgca tcataacgca acgccgcgaa 600
ggcttctgct cctcttcaag ctgtagatgc tgtcaatctt gctgccctcg gggctctgtg 660
gcatccgtta actttgcttt tccgggaaga aaaatgtctt gtgctaagct ccacccctcg 720
aatgcggcgg tgggccagga tttatgtcta catccagcct atacttctcc tgg 773

<210> 39
<211> 852
<212> DNA
<213> Murinae

<400> 39
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tcaagaggct gtgggcaacg ttgtgctcct ggcccttgtc accctcatca gcgtggtcca 120
gaatgtgttt tttgcccact atgtggagca tgaaagcaat gcgcataatg ggagaagctt 180
ccagaggacc gggactcttg cctttgagcg ggtctacact gccaaccaga actgcgtaga 240
tgcgtacccc actttccttg tggtactctg gactgcagga ctactttgca gccaagtccc 300
tgccgccttc gccggactga tgtacctgtt tgtgaggcaa aaatactttg tcggctatct 360
gggagagaga actcagagca cccctggcta catcttcggc aagcggatca tcctgttcct 420
gttcctcatg tccttcgccg ggatactcaa ccattacctc atcttcttct tcggaagcga 480
ctttgagaac tacatcagaa cggtaagcac gacgatctcc ccgctgcttc tcatcccctg 540
attgctggag acagagaagg acgctcacca gatcaataga gacgcatcat aacgcaacgc 600
cgcgaaggct tctgctcctc ttcaagctgt agatgctgtc aatcttgctg ccctcggggc 660
tctgtggcat ccgttaactt tgcttttccg ggaagaaaaa tgtcttgtgc tagctccacc 720
cctcgaatgc ggcggtggcc caggatttat tgtctacatc cagcctatac ttctcctggc 780
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tagacaaaat tt 852

<210> 40
<211> 161
<212> PRT
<213> Murinae

<400> 40
Met Asp Gln Glu Ala Val Gly Asn Val Val Leu Leu Ala Leu Val Thr
 1   5   10   15
Leu Ile Ser Val Val Gln Asn Val Phe Phe Ala His Tyr Val Glu His
            20   25   30
Glu Ser Asn Ala His Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
        35   40   45
Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
    50   55   60
Pro Thr Phe Leu Val Val Leu Trp Thr Ala Gly Leu Leu Cys Ser Gln
65   70   75   80
Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
                85   90   95
Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
            100   105   110
Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Phe Ala
        115   120   125
Gly Ile Leu Asn His Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
    130   135   140
Asn Tyr Ile Arg Thr Val Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145   150   155   160
Pro

<210> 41
<211> 873

<212> DNA
<213> Homo sapiens

<400> 41
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agcctgaagc aaacatggat caagaaactg taggcaatgt tgtcctgttg gccatcgtca 120
ccctcatcag cgtggtccag aatggattct ttgcccataa agtggagcac gaaagcagga 180
cccagaatgg gaggagcttc cagaggaccg gaacacttgc ctttgagcgg gtctacactg 240
ccaaccagaa ctgtgtagat gcgtacccca ctttcctcgc tgtgctctgg tctgcggggc 300
tactttgcag ccaagttcct gctgcgtttg ctggactgat gtacttgttt gtgaggcaaa 360
agtactttgt cggttaccta ggagagagaa cgcagagcac ccctggctac atatttggga 420
aacgcatcat actcttcctg ttcctcatgt ccgttgctgg catattcaac tattacctca 480
tcttcttttt cggaagtgac tttgaaaact acataaagac gatctccacc accatctccc 540
ctctacttct cattccctaa ctctctgctg aatatggggt tggtgttctc atctaatcaa 600
tacctacaag tcatcataat tcagctcttg agagcattct gctcttcttt agatggctgt 660
aaatctattg gccatctggg cttcacagct tgagttaacc ttgcttttcc gggaacaaaa 720
tgatgtcatg tcagctccgc cccttgaaca tgaccgtggc cccaaatttg ctattcccat 780
gcattttgtt tgtttcttca cttatcctgt tctctgaaga tgttttgtga ccaggtttgt 840
gttttcttaa aataaaatgc agagacatgt ttt 873

<210> 42
<211> 161
<212> PRT
<213> Homo sapiens

<400> 42
Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr
 1   5   10   15
Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His
            20   25   30
Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
        35   40   45
Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
    50   55   60
Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln
65   70   75   80
Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
                85   90   95
Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
            100   105   110
Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala
        115   120   125
Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
    130   135   140
Asn Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145   150   155   160
Pro

<210> 43
<211> 803
<212> DNA
<213> Murinae

<400> 43
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tcatggattt tctcgaccag aaaatcagac tattttcctg aataatctac tagaaacttt 120
tacggaacac atttcatgtt tcctttgaag agttaagaga agaaagtatt tgtaagaaca 180
ggaaaagaaa caaatacttt gcaaataaac tggctgctgc tgtgaccaca tctgaatagc 240
aaaggcgatc gatcaagcgc tgcggacaaa aggcctcctg taagctgcac tgcctgacaa 300
tggtaagctc caatggctcc cagtgccctt atgacgactc ctttaagtac actctgtacg 360
ggtgcatgtt cagcatggtc ttcgtgcttg ggctgatatc caactgtgtt gcgatataca 420
ttttcatctg tgccctcaaa gtgagaaatg aaactacaac gtacatgatt aacctggcaa 480
tgtcagattt acttttcgtc tttactttgc catttcggat tttttacttt gcaacacgga 540
attggccatt tggagatcta ctctgtaaga tttcagtaat gctgttttac accaatatgt 600
atgggaagca ttctgttctt aacctgtatc agtgtagatc gatttctggc aattgtctac 660
ccatttaagt caaagacttt aagaaacgaa acgaaaatgc aaagaatcgt ttgcattgcc 720
tgtgtggttc acagtgatgg gaggaagtgc gctgcagttt tctttcagtc gacccactct 780
caggggaaca atactcagaa gct 803

<210> 44
<211> 1849
<212> DNA
<213> Murinae

<400> 44
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cgcgaacatg cttaggaatt tatctgggat cccttaaacg actgcctatc gccgtccgga 120
atcaatgtag aaatacaaag tttgagaata aaaagaagga agaagtaccc gaggacgacg 180
ggcggacgga cgcacggcga gtgtttgtga ctgaagtaaa gctggtttgg accctggcgg 240
ctgaagcaca agtttccacg cggactggtc tggtccgact tggaacagtt tttccttaca 300
ctttcagctt tatgggttgg cttccttgac tgcattttct gtcagttaac taaactccag 360
actcatggat tttctcgacc agaaaatcag actattttcc tgaataatct actagaaact 420
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caggaaaaga aacaaatact ttgcaaataa actggctgct gctgtgacca catctgaata 540
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aatggtaagc tccaatggct cccagtgccc ttatgacgac tcctttaagt acactctgta 660
cgggtgcatg ttcagcatgg tcttcgtgct tgggctgata tccaactgtg ttgcgatata 720
cattttcatc tgtgccctca aagtgagaaa tgaaactaca acgtacatga ttaacctggc 780
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<210> 45

<211> 316
<212> PRT
<213> Murinae

<400> 45
Asp Asp Ser Phe Lys Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val
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Phe Val Leu Gly Leu Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile
            20   25   30
Cys Ala Leu Lys Val Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu
        35   40   45
Ala Met Ser Asp Leu Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe
    50   55   60
Tyr Phe Ala Thr Arg Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile
65   70   75   80
Ser Val Met Leu Phe Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu
                85   90   95
Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys
            100   105   110
Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala Lys Ile Val Cys Ile Ala
        115   120   125
Val Trp Phe Thr Val Met Gly Gly Ser Ala Pro Ala Val Phe Phe Gln
    130   135   140
Ser Thr His Ser Gln Gly Asn Asn Thr Ser Glu Ala Cys Phe Glu Asn
145   150   155   160
Phe Pro Ala Ala Thr Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe
                165   170   175
Ile Glu Ile Val Gly Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys
            180   185   190
Ser Ser Met Val Leu Arg Thr Leu Asn Lys Pro Val Thr Leu Ser Arg
        195   200   205
Ser Lys Met Asn Lys Thr Lys Val Leu Lys Met Ile Phe Val His Leu
    210   215   220
Val Ile Phe Cys Phe Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu
225   230   235   240
Tyr Ser Leu Met Arg Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala
                245   250   255
Ala Val Arg Thr Met Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn
            260   265   270
Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln
        275   280   285
Asn Ser Ile Lys Met Lys Asn Trp Ser Val Arg Arg Ser Asp Ser Arg
    290   295   300
Phe Ser Glu Val Gln Gly Thr Glu Asn Phe Ile Gln
305   310   315

<210> 46
<211> 1035
<212> DNA
<213> Homo sapiens

<400> 46
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gggtgcatgt tcagcatggt gtttgtgctt gggttaatat ccaattgtgt tgccatatac 120

attttcatct gcgtcctcaa agtccgaaat gaaactacaa cttacatgat taacttggca 180
atgtcagact tgctttttgt ttttacttta cccttcagga ttttttactt cacaacacgg 240
aattggccat ttggagattt actttgtaag atttctgtga tgctgtttta taccaacatg 300
tacggaagca ttctgttctt aacctgtatt agtgtagatc gatttctggc aattgtctac 360
ccatttaagt caaagactct aagaaccaaa agaaatgcaa agattgtttg cactggcgtg 420
tggttaactg tgatcggagg aagtgcaccc gccgtttttg ttcagtctac ccactctcag 480
ggtaacaatg cctcagaagc ctgctttgaa aattttccag aagccacatg gaaaacatat 540
ctctcaagga ttgtaatttt catcgaaata gtgggatttt ttattcctct aattttaaat 600
gtaacttgtt ctagtatggt gctaaaaact ttaaccaaac ctgttacatt aagtagaagc 660
aaaataaaca aaactaaggt tttaaaaatg atttttgtac atttgatcat attctgtttc 720
tgttttgttc cttacaatat caatcttatt ttatattctc ttgtgagaac acaaacattt 780
gttaattgct cagtagtggc agcagtaagg acaatgtacc caatcactct ctgtattgct 840
gtttccaact gttgttttga ccctatagtt tactacttta catcggacac aattcagaat 900
tcaataaaaa tgaaaaactg gtctgtcagg agaagtgact tcagattctc tgaagttcat 960
ggtgcagaga attttattca gcataaccta cagaccttaa aaagtaagat atttgacaat 1020
gaatctgctg cctga 1035

<210> 47
<211> 344
<212> PRT
<213> Homo sapiens

<400> 47
Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys
 1   5   10   15
Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu
            20   25   30
Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val
        35   40   45
Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu
    50   55   60
Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg
65   70   75   80
Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe
                85   90   95
Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val
            100   105   110
Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg
        115   120   125
Thr Lys Arg Asn Ala Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val
    130   135   140
Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln
145   150   155   160
Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr
                165   170   175
Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly
            180   185   190
Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu
        195   200   205
Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys
    210   215   220
Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe
225   230   235   240
Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg
                245   250   255

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Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met
            260                 265                 270
Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro
        275                 280                 285
Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met
    290                 295                 300
Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His
305                 310                 315                 320
Gly Ala Glu Asn Phe Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys
                325                 330                 335
Ile Phe Asp Asn Glu Ser Ala Ala
            340
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<210> 48
<211> 814
<212> DNA
<213> Murinae

<400> 48
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ggccaggcct agcacatgta cctcacagac caactggcaa gcagccttca gggagctcga 120
tccccaaaca gccagtcacc acctctgtcc cctcttcact gttggtcgtc agactgcctg 180
agtggacagc aggctggtcg cgttgtattt tcacttcctt cctctgactg gcttgctctt 240
gtctctcagt ctttcatccc aggcagctgc ctgaggtagg tgaggaggat ggtgagccag 300
gcaggtctac aataaaggca gctctgtccg gctccttctg gctcgtgagt gtcaccggcc 360
tggaagactg agggaatggc tcccctctct cctccccgtc tttccccagt tccttcccta 420
tgttggccca tgtgcccagg gagttggaag catcagggag accctcttag tgtggggaag 480
gaagtcagag accattgaca cagtgaagag gcaggatcat gtgttggaag cctgttagca 540
ggaccaaggt gactcttggg agagactctt gtggacacag gccgtggtgg cttgtcagac 600
cttaaagggt ccaggcccac ccctgccagg atccctggtc tgctttctcc aggacacact 660
gggacactgc tgagtaatga gcagcttatt acacacaatg ggaagagggg cagagagggc 720
tgtgtcggtt gagtctcggc tgggactgaa gtttgccata agtagtggtt gtacatccag 780
gagcctggct acctgtcttt acccccttgaa ggac 814

<210> 49
<211> 1164
<212> DNA
<213> Murinae

<400> 49
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cagcccagcc tcttggggtt caggagggtc ctgcagaaac tccagacgga cggactcaag 180
gagtgcatta tcttctgcgt gcgggaggag cctgtggtgt tcttgcgcgc tgaggaggac 240
tttgtgtctt acacacctcg agacaaggag agccttcatg agaacctcag ggaccctagt 300
ccaggggtca aggctgagaa tctggagctg gccatccaga aagagatcca tgactttgcc 360
caattgagag ataatgtgta ccacgtatac cacaacacag aggacctgcg cggggagccg 420
cacaccgtgg ccatccgagg tgaggatggc gtgtgcgtga ccgaggaggt gtttaagcgg 480
ccgctcttcc tgcagcccac ctacagatac caccgcctcc ccttgccaga gcaaggggcc 540
cccctggaag cccagtttga tgcctttgtc agcgttcttc gggagacccc cagccttctg 600
ccactcagag ataaccacgg gcctctgcct gccctcctgt tcagctgcca gtcaggtgta 660
ggcagaacca acctaggcat ggtcctggga accctcgtca tgttccacca cagtaggacc 720
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gtgatccagg gcttcatctg taaggtgcca caggggaaga aaatggtgga ggaggtggat 840

cgagcgatca gtgcctgtgc agagttgcat gacctgaagg aggaggtcct aaaaaaccag 900
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tatctgcatg agcagtaccc cctggccttt gccctcagtt tcagtcgatg gctgtgtacc 1080
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gacctcatcg ccaagggctc cctg 1164

<210> 50
<211> 388
<212> PRT
<213> Murinae

<400> 50
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20 25 30
Gly Leu Pro Val Phe Gly Met Gly Gln Pro Ser Leu Leu Gly Phe Arg
35 40 45
Arg Val Leu Gln Lys Leu Gln Thr Asp Gly Leu Lys Glu Cys Ile Ile
50 55 60
Phe Cys Val Arg Glu Glu Pro Val Val Phe Leu Arg Ala Glu Glu Asp
65 70 75 80
Phe Val Ser Tyr Thr Pro Arg Asp Lys Glu Ser Leu His Glu Asn Leu
85 90 95
Arg Asp Pro Ser Pro Gly Val Lys Ala Glu Asn Leu Glu Leu Ala Ile
100 105 110
Gln Lys Glu Ile His Asp Phe Ala Gln Leu Arg Asp Asn Val Tyr His
115 120 125
Val Tyr His Asn Thr Glu Asp Leu Arg Gly Glu Pro His Thr Val Ala
130 135 140
Ile Arg Gly Glu Asp Gly Val Cys Val Thr Glu Glu Val Phe Lys Arg
145 150 155 160
Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg Leu Pro Leu Pro
165 170 175
Glu Gln Gly Ala Pro Leu Glu Ala Gln Phe Asp Ala Phe Val Ser Val
180 185 190
Leu Arg Glu Thr Pro Ser Leu Leu Pro Leu Arg Asp Asn His Gly Pro
195 200 205
Leu Pro Ala Leu Leu Phe Ser Cys Gln Ser Gly Val Gly Arg Thr Asn
210 215 220
Leu Gly Met Val Leu Gly Thr Leu Val Met Phe His His Ser Arg Thr
225 230 235 240
Thr Ser Gln Leu Glu Ala Ala Ser Pro Leu Ala Lys Pro Leu Pro Met
245 250 255
Glu Gln Phe Gln Val Ile Gln Gly Phe Ile Cys Lys Val Pro Gln Gly
260 265 270
Lys Lys Met Val Glu Glu Val Asp Arg Ala Ile Ser Ala Cys Ala Glu
275 280 285
Leu His Asp Leu Lys Glu Glu Val Leu Lys Asn Gln Arg Arg Leu Glu
290 295 300
Ser Phe Arg Pro Glu Ser Arg Gly Gln Glu Cys Gly Ser Gln Gln Ala
305 310 315 320
Val Gln Gln Arg Ala Leu Trp Ser Leu Glu Leu Tyr Phe Tyr Leu Leu
325 330 335

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Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu Ala Phe Ala Leu
            340                 345                 350
Ser Phe Ser Arg Trp Leu Cys Thr His Pro Glu Leu Tyr Arg Leu Leu
        355                 360                 365
Val Glu Leu Asn Ser Val Gly Pro Leu Val Pro Gly Asp Leu Ile Ala
    370                 375                 380
Lys Gly Ser Leu
385
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<210> 51
<211> 4303
<212> DNA
<213> Homo sapiens

<400> 51
ggctgctggc agactatggg tacaacggcc agcacagccc agcagacggt ctcggcaggc 60
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cactccttcc agagcactag cttgcataac agcaaggcca agtccatcat ccccaacaag 180
gtggcccctg ttgtgatcac gtacaactgc aaggaggagt tccagatcca tgatgagctg 240
ctcaaggctc attacacgtt gggccggctc tcggacaaca cccctgagca ctacctggtg 300
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<210> 52
<211> 861
<212> PRT
<213> Homo sapiens

<400> 52

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            20                  25                  30
Asp Ser Arg His Ser Val Ser Ile His Ser Phe Gln Ser Thr Ser Leu
        35                  40                  45
His Asn Ser Lys Ala Lys Ser Ile Ile Pro Asn Lys Val Ala Pro Val
    50                  55                  60
Val Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu
65                  70                  75                  80
Leu Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu
                85                  90                  95
His Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu
            100                 105                 110
Lys Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe
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        115                 120                 125
Arg Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser
    130                 135                 140
Leu Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His
145                 150                 155                 160
Arg Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu
                165                 170                 175
Arg Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn
            180                 185                 190
Leu His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser
        195                 200                 205
Leu Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser
    210                 215                 220
Glu Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu
225                 230                 235                 240
Pro His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu
                245                 250                 255
Glu Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His
            260                 265                 270
Arg Leu Pro Leu Pro Glu Gln Gly Ser Pro Leu Glu Ala Gln Leu Asp
        275                 280                 285
Ala Phe Val Ser Val Leu Arg Glu Thr Pro Ser Leu Leu Gln Leu Arg
    290                 295                 300
Asp Ala His Gly Pro Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly
305                 310                 315                 320
Val Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu
                325                 330                 335
His Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala
            340                 345                 350
Lys Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg
        355                 360                 365
Met Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile
    370                 375                 380
Thr Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn
385                 390                 395                 400
Gln Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser
                405                 410                 415
Gly Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg
            420                 425                 430
Tyr Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro
        435                 440                 445
Leu Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu
    450                 455                 460
Leu Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro
465                 470                 475                 480
Arg Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser
                485                 490                 495
Pro Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg
            500                 505                 510
Arg Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys
        515                 520                 525
Ala Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu
    530                 535                 540
Arg Lys Val Val Trp Val Ser Leu Arg Glu Glu Ala Val Leu Glu Cys
545                 550                 555                 560
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Asp Gly His Thr Tyr Ser Leu Arg Trp Pro Gly Pro Pro Val Ala Pro
                565                 570                 575
Asp Gln Leu Glu Thr Leu Glu Ala Gln Leu Lys Ala His Leu Ser Glu
            580                 585                 590
Pro Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys
        595                 600                 605
Leu Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly
    610                 615                 620
Leu Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu
625                 630                 635                 640
Glu Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys
                645                 650                 655
Asp Pro Gly Thr Gly Phe Val Phe Ser Cys Leu Ser Gly Gln Gly Arg
            660                 665                 670
Thr Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln
        675                 680                 685
Gly Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala
    690                 695                 700
Lys Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu
705                 710                 715                 720
Leu Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp
                725                 730                 735
Thr Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile
            740                 745                 750
Ile Ile Cys Thr Tyr Arg Gln Ala Lys Ala Ala Lys Glu Ala Gln Glu
        755                 760                 765
Met Arg Arg Leu Gln Leu Arg Ser Leu Gln Tyr Leu Glu Arg Tyr Val
    770                 775                 780
Cys Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser
785                 790                 795                 800
Trp Gln Arg Pro Phe Ser Thr Trp Met Gln Glu Val Ala Ser Lys Ala
                805                 810                 815
Gly Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser
            820                 825                 830
Gly Glu Asp Gln Pro Phe Ser Arg Leu Arg Tyr Arg Trp Gln Glu Gln
        835                 840                 845
Ser Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu
    850                 855                 860
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